Quantitative MR imaging of brain tumors: A step forward?

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Introduction

A quantitative analysis of different diagnostic methods provides more precise information of the nature and the extent of a pathology in patients with intracranial tumors and thus improves outcome from magnetic resonance (MR) examination of patients. Coregistration of MR spectroscopic (SI), diffusion and relaxation images and their subsequent correlations based on multivoxel methods are primary used to assess the tumor extent [1,2], as they have a potential to distinguish pathological states - a tumor, edema, tumor infiltrated edema, necrosis - and a healthy tissue. Therefore, we decided to perform a prospective quantitative MR study of patients suffering from brain tumors - low and high grade gliomas (LGG, HGG resp.), lymphomas (LYM), recurrent tumors and tissue changes caused by radiation therapy - to validate these promising techniques and their potential use in the clinical routine.

Subjects and Methods

41 patients with a diagnosis of an intracranial tumor and 55 healthy subjects were examined using a 3T imager equipped with a Tx/Rx head coil. The patients were divided into 2 groups. The group 1 consisted of 24 patients with untreated brain lesions. The group 2 consisted of 17 patients with a tumor recurrence or radiation necrosis after resection of a primary brain tumor and consequent chemotherapy and radiotherapy. A diagnosis of 18 untreated patients was assessed by image-guided stereotactic biopsy performed within 2 days after MR examination. The diagnosis of 14 patients was assessed from the open-frame navigated biopsy during subtotal or total lesion resection. The diagnosis of radiation changes in remaining patients was assessed by radiologist after at least 6 months-follow-up.

The measurement protocol consists of anatomical T2-weighted MR images, SI (2D PRESS-SI, 16x16, FOV=160x160x15mm, TR/TE/NA=1510ms/30 and 135ms/4), DTI (EPI-SE, TR/TE/NA=7100ms/98ms/3, 20 directions, b=0,1000s/mm^2, slice thickness (st) 2.5mm), T2 relaxometry (CPMG, TR/TE/NA=3000/13.2-422.4/1, 32 echoes, st=5mm). SI data were analyzed by a program SIPRO [3], relaxation data by an in-house program ViDi utilizing a three-parameter fit, mean diffusivity (MD) by a program FSL and correlations by a program CORIMA [1] with automatic identification of pixels in the normal tissue according to control data.

All the subjects provided an informed consent. Clinical protocols are certificated according to the ISO 9001:2008 norm.

Results/Discussion

Different correlations between metabolic concentrations and mean diffusivity and T2 relaxation times (T2) were found not only for different lesion localization, but also for different tumor types. The origin of special correlation patterns of choline(Cho)-MD and Cho-T2 (see Figure 1, pattern A in LGG, C in HGG and E in LYM) is based on a different tissue state involved in an examined area, i.e. healthy tissue (region 1), tissue infiltrated by tumorous cells (region 2), active tumor (region 3), tumor infiltrated edema (region 4), edema (region 5), etc. The positive linear MD-T2 correlation was found in LGG and LYM (Fig.1, patterns B, D), not in HGG (pattern F). Recurrent tumors exhibit the same correlation patterns as untreated ones, but with changed metabolic values caused by radiation/ chemotherapy. Metabolic values do not correlate with MD and T2 in the tissue with radiation changes only. Correlations of the following MR parameters are suitable for tissue differentiation: MD, T2, Cho, N-acetyl aspartate, creatine, inositol, lactate, macromolecules and lipids and metabolite ratios.

Although the technique can be used only in semiautomatic mode due to an unavoidable chemical shift artifact in SI and image distortions in DTI, we showed that the combination of different MR parameters is able to describe the complexity of a highly heterogeneous tissue in the tumor and in its vicinity. As an edematous tissue is characterized by similar Cho, MD and T2 values as in the healthy gray matter, the whole set of different correlations has to be considered for its differentiation. The special MD-T2 pattern F (Fig.1) differentiating HGG from LGG and LYM is caused by a dense non-enhancing tissue in the proximity of HGG. We therefore hypothesize that the high cellular tumor shrinks extracellular space (leading to low MD) due to high tumor cellularity and simultaneously causes a cellular swelling leading to an increased water content in the intracellular space (and increase of T2).

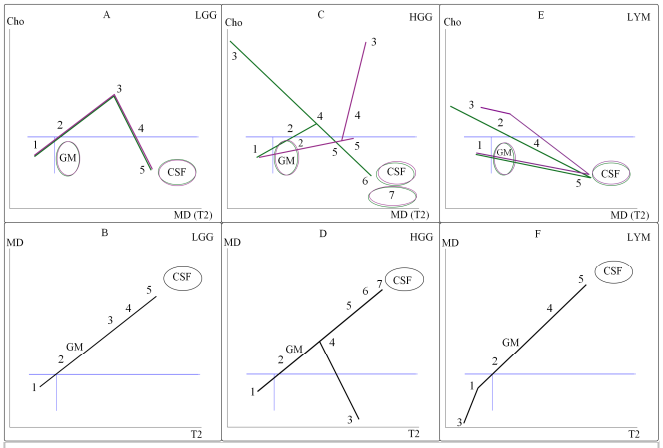

Fig. 1: Schematic correlations in LGG, HGG and LYM. Cho-MD (green), Cho-T2 (violet) correlations are in the first row, MD-T2 in the second one. Region 1 corresponds to a healthy tissue, 2 - infiltrative tumor, 3 - active tumor, 4 - tumor infiltrated edema, 5 - edema, 6 - tumor/ necrosis, 7 - necrotic tissue, GM - gray matter; CSF - cerebrospinal fluid.

Conclusion

We showed that a combination of different MR parameters based on pixel-by-pixel basis and their correlations in individual patients may help in better identification of the tumor type, examination of the tumor extension, direction of proliferation and also in better understanding of biochemical processes inside the tumor.

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[2] Khayal IS et al. J Magn Reson Imaging 2008; 27:718–725,
[3] http://www.sites.google.com/site/jsiprotool/

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